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RAW SEQUENCE LISTING   DATE: 12/26/2002
PATENT APPLICATION: **US/09/846,637C**   TIME: 13:32:53

Input Set : **A:\2502seq.003**
Output Set: **N:\CRF4\12262002\I846637C.raw**

```
 3 <110> APPLICANT: Jensen, Michael
 5 <120> TITLE OF INVENTION: Selection Systems for Genetically
 6       Modified Cells
 8 <130> FILE REFERENCE: 24751-2502
10 <140> CURRENT APPLICATION NUMBER: US/09/846,637C
11 <141> CURRENT FILING DATE: 2001-04-30
13 <160> NUMBER OF SEQ ID NOS: 40
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1654
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapien
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (48)...(1589)
25 <223> OTHER INFORMATION: Human Wild-type Inosine Monophospate Dehydrogenase
26       II (IMPDH II)
28 <300> PUBLICATION INFORMATION:
29 <301> AUTHORs: Collart,F.R. and Huberman,E.
30 <302> TITLE: Cloning and sequence analysis of the human and
31 <303> JOURNAL: J. Biol. Chem. (1988)
32 <304> VOLUME: 263
33 <306> PAGES: 15769-15772
35 <400> SEQUENCE: 1
36 gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac         56
37                                                         Met Ala Asp
38                                                          1
40 tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca        104
41 Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
42      5                  10                  15
44 gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt        152
45 Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
46  20                  25                  30                  35
48 ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg        200
49 Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
50                  40                  45                  50
52 act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc        248
53 Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
54                  55                  60                  65
56 tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg        296
57 Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
58              70                  75                  80
60 ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc        344
```

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```
61 Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
62      85              90                95
64 cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc    392
65 Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile
66 100             105             110                 115
68 aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt    440
69 Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe
70              120             125             130
72 gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca    488
73 Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr
74              135             140             145
76 ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att    536
77 Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile
78              150             155             160
80 gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg    584
81 Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met
82      165             170             175
84 aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag    632
85 Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile Thr Leu Lys
86 180             185             190                 195
88 gag gca aat gaa att ctg cag cgc agc aag aag gga aag ttg ccc att    680
89 Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu Pro Ile
90              200             205             210
92 gta aat gaa gat gat gag ctt gtg gcc atc att gcc cgg aca gac ctg    728
93 Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg Thr Asp Leu
94              215             220             225
96 aag aag aat cgg gac tac cca cta gcc tcc aaa gat gcc aag aaa cag    776
97 Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala Lys Lys Gln
98      230             235             240
100 ctg ctg tgt ggg gca gcc att ggc act cat gag gat gac aag tat agg   824
101 Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys Tyr Arg
102     245             250             255
104 ctg gac ttg ctc gcc cag gct ggt gtg gat gta gtg gtt ttg gac tct   872
105 Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp Ser
106 260             265             270                 275
108 tcc cag gga aat tcc atc ttc cag atc aat atg atc aag tac atc aaa   920
109 Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr Ile Lys
110             280             285             290
112 gac aaa tac cct aat ctc caa gtc att gga ggc aat gtg gtc act gct   968
113 Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr Ala
114             295             300             305
116 gcc cag gcc aag aac ctc att gat gca ggt gtg gat gcc ctg cgg gtg   1016
117 Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg Val
118             310             315             320
120 ggc atg gga agt ggc tcc atc tgc att acg cag gaa gtg ctg gcc tgt   1064
121 Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys
122     325             330             335
124 ggg cgg ccc caa gca aca gca gtg tac aag gtg tca gag tat gca cgg   1112
125 Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr Ala Arg
```

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Input Set : **A:\2502seq.003**
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```
126 340                   345                350                  355
128 cgc ttt ggt gtt ccg gtc att gct gat gga gga atc caa aat gtg ggt    1160
129 Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val Gly
130               360                365                  370
132 cat att gcg aaa gcc ttg gcc ctt ggg gcc tcc aca gtc atg atg ggc    1208
133 His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met Gly
134               375                380                  385
136 tct ctc ctg gct gcc acc act gag gcc cct ggt gaa tac ttc ttt tcc    1256
137 Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe Ser
138               390                395                  400
140 gat ggg atc cgg cta aag aaa tat cgc ggt atg ggt tct ctc gat gcc    1304
141 Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu Asp Ala
142       405                410                415
144 atg gac aag cac ctc agc agc cag aac aga tat ttc agt gaa gct gac    1352
145 Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp
146 420                   425                430                  435
148 aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac aaa ggg    1400
149 Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys Gly
150               440                445                  450
152 tca atc cac aaa ttt gtc cct tac ctg att gct ggc atc caa cac tca    1448
153 Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln His Ser
154               455                460                  465
156 tgc cag gac att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg    1496
157 Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met
158               470                475                  480
160 tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg    1544
161 Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val
162       485                490                495
164 gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc       1589
165 Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
166 500                   505                510
168 tgaaaaggga tccagcacac ctcctcggtt tttttttcaa taaaagttta gaaagacccg    1649
169 aattc                                                               1654
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 514
173 <212> TYPE: PRT
174 <213> ORGANISM: Homo sapien
176 <400> SEQUENCE: 2
177 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
178  1               5                10                   15
179 Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
180               20                25                   30
181 Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
182       35                40                   45
183 Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
184       50                55                   60
185 Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
186 65                70                   75                   80
187 Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
```

RAW SEQUENCE LISTING   DATE: 12/26/2002
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Input Set : **A:\2502seq.003**
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```
188                 85                  90                  95
189 Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
190             100                 105                 110
191 Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
192         115                 120                 125
193 Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
194         130                 135                 140
195 Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
196 145                 150                 155                 160
197 Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
198             165                 170                 175
199 Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile
200             180                 185                 190
201 Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
202         195                 200                 205
203 Leu Pro Ile Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg
204         210                 215                 220
205 Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
206 225                 230                 235                 240
207 Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
208             245                 250                 255
209 Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val
210         260                 265                 270
211 Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
212         275                 280                 285
213 Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
214     290                 295                 300
215 Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
216 305                 310                 315                 320
217 Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val
218             325                 330                 335
219 Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
220         340                 345                 350
221 Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
222         355                 360                 365
223 Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
224     370                 375                 380
225 Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
226 385                 390                 395                 400
227 Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
228             405                 410                 415
229 Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
230         420                 425                 430
231 Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
232         435                 440                 445
233 Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
234     450                 455                 460
235 Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
236 465                 470                 475                 480
```

```
237 Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
238                 485                 490                 495
239 Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
240             500                 505                 510
241 Leu Phe
244 <210> SEQ ID NO: 3
245 <211> LENGTH: 1654
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo sapien
249 <220> FEATURE:
250 <221> NAME/KEY: CDS
251 <222> LOCATION: (48)...(1589)
252 <223> OTHER INFORMATION: T333I/S351Y Human IMPDH II mutant
254 <221> NAME/KEY: mutation
255 <222> LOCATION: 1045
256 <223> OTHER INFORMATION: C to T mutation
```

W--> 258 <221> mutation
```
259 <222> LOCATION: 1046
260 <223> OTHER INFORMATION: G to C mutation
```
W--> 262 <221> mutation
```
263 <222> LOCATION: 1099
264 <223> OTHER INFORMATION: C to A mutation
```
W--> 266 <221> mutation
```
267 <222> LOCATION: 1100
268 <223> OTHER INFORMATION: A to T mutation
```
W--> 270 <400> 3
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271 gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac      56
272                                                     Met Ala Asp
273                                                       1
275 tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca     104
276 Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
277       5                  10                  15
279 gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt     152
280 Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
281  20                  25                  30                  35
283 ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg     200
284 Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
285                  40                  45                  50
287 act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc     248
288 Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
289             55                  60                  65
291 tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg     296
292 Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
293             70                  75                  80
295 ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc     344
296 Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
297             85                  90                  95
299 cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc     392
300 Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile
```

VERIFICATION SUMMARY   DATE: 12/26/2002
PATENT APPLICATION: **US/09/846,637C**   TIME: 13:32:54

Input Set : **A:\2502seq.003**
Output Set: **N:\CRF4\12262002\I846637C.raw**

```
L:258  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:262  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:266  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:270  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:500  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:730  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:953  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:965  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:1188 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:1199 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:2109 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:19, CDS LOCATION: (0)...
(1188)
L:2462 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:2473 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:2634 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25
L:2855 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:27
L:3297 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:31
L:3301 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:31
```